

sequence which has promoter activity from the 5' flanking region of genomic DNA which specifically hybridizes to said probe, wherein] the group consisting of:

a) nucleotides 65-4163 of SEQ ID NO:7,

b) SEQ ID NO:15, and

c) a DNA sequence which hybridizes with SEQ ID NO:15 or nucleotides 65-4163 of SEQ ID NO:7 under conditions comprising hybridization [is carried out] in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and [hybridization washes are performed] washing in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes[, whereby said transcriptional factor is obtained].

- 2. (Reiterated) The DNA sequence according to Claim 1, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.
- 3. (Reiterated) The DNA sequence according to Claim 2, wherein said transport signal encoding sequence comprises a plastid transit peptide.
- 4. (Reiterated) The DNA sequence according to Claim 1, wherein said DNA sequence further comprises as an operably joined component a transport signal encoding sequence for a signal peptide which provides for transport across the rough endoplasmic reticulum.
- 5. (Reiterated) The DNA sequence according to Claim 4, wherein said DNA sequence further comprises as an operably joined component, 3' to said open reading frame, a vacuolar localization signal.
- 7. (Reiterated) The DNA sequence of Claim 1 wherein said open reading frame is from a bacterial or a plant gene.



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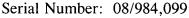
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- 8. (Reiterated) The DNA sequence of Claim 7 wherein said gene is selected from the group consisting of ORF438, *tyr*A, anthocyanin R gene, anthocyanin C1 gene, *pig*, and *tna*.
- 9. (Reiterated) A DNA construct comprising a DNA sequence of Claim 1.
- 10. (Reiterated) A DNA construct comprising two DNA sequences according to Claim 1, wherein said protein in a biosynthesis pathway in each of said two DNA sequences is not encoded by the same gene.
- 12. (Reiterated) A plant cell comprising a DNA construct of Claim 9.
- 13. (Reiterated) A plant comprising a cell of Claim 12.

14. (Twice Amended) A method of modifying fiber phenotype in a cotton plant, said method comprising:

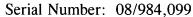
transforming a plant cell with a DNA construct according to Claim 9 or 10; and growing said plant cell to produce a plant comprising [said] fiber tissue, wherein said [plant] fiber tissue comprises a substrate of said protein [of interest] in a pigment biosynthesis pathway, and wherein said protein reacts with said substrate to produce said pigment, whereby the phenotype of said fiber is modified.

- 15. (Reiterated) The method of Claim 14 wherein said DNA construct further comprises a transport signal encoding sequence from a plant nuclear-encoded gene.
- 16. (Reiterated) The method of Claim 14 wherein said DNA construct further comprises a transport signal encoding sequence, which encodes a signal peptide which provides for transport across the rough endoplasmic reticulum.



- 18. (Reiterated) The method of Claim 16 wherein said DNA comprises constructs for expression of two proteins in a pigment biosynthesis pathway wherein said two proteins are not encoded by the same gene.
- 19. (Reiterated) The method of Claim 18 wherein said pigment is melanin and said proteins are encoded by *tyr*A and ORF438.
- 20. (Reiterated) The method of Claim 18 wherein said pigment is indigo and said proteins are encoded by *tna* and *pig*.
- 21. (Reiterated) The method of Claim 18 wherein said pigment is anthocyanin and said two proteins are the anthocyanin R and C1 proteins.
- 22. (Reiterated) The method of Claim 14 wherein said fiber tissue is a cotton burr.
- 23. (Allowable) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in SEQ ID NO: 7.
- 24. (Allowable) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in SEQ ID NO: 15.
- 25. (Allowable) An isolated DNA comprising the nucleotide sequence shown in SEQ ID NO: 1.
- 26. (Allowable) An isolated DNA comprising the nucleotide sequence shown in SEQ ID NO: 12.

Cancel Claim 27.



28. (Amended) The DNA sequence according to Claim 1, wherein said <u>transcriptional</u> factor is obtained by the method of probing a genomic library derived from a plant fiber tissue [is cotton fiber tissue].

- 30. (Reiterated) The DNA sequence according to Claim 59, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.
- 31. (Reiterated) The DNA sequence according to Claim 30, wherein said transport signal encoding sequence comprises a plastid transit peptide.
- 32. (Reiterated) The DNA sequence according to Claim 59, further comprising a transport signal encoding sequence for a signal peptide which provides for transport across the rough endoplasmic reticulum.
- 33. (Reiterated) The DNA sequence according to Claim 32, wherein said sequence further comprises, 3' to said open reading frame, a vacuolar localization signal.
- 34. (Reiterated) The DNA sequence of Claim 57 wherein said open reading frame is from a bacterial gene.
- 35. (Amended) The DNA sequence of Claim 34 wherein said <u>bacterial</u> gene is selected from the group consisting of ORF438, *tyrA*, *pig*, and *tna*.
 - 36. (Reiterated) A DNA construct comprising a DNA sequence of Claim 59.
- 3331. (Amended) The DNA construct of Claim 36 wherein said cotton plant cell is a cotton fiber cell.

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- 38. (Reiterated) A plant cell comprising a DNA construct of Claim 36.
- 39. (Reiterated) A plant comprising a plant cell of Claim 38.

42. (Twice Amended) The DNA sequence according to Claim 59 wherein said transcriptional factor is obtained by the method of probing a genomic library derived from a plant fiber tissue [is cotton fiber tissue].

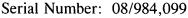
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44. (Twice Amended) A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional factor functional in a cotton [fiber] plant cell and an open reading frame encoding an enzyme in a biosynthetic [or degradation] pathway of melanin or indigo, wherein said transcriptional factor is [obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the fall length of a probe derived from the cDNA sequence shown in SEQ ID NO: 1 or SEQ ID NO: 7 or SEQ ID NO: 11 or SEQ ID NO: 12 or SEQ ID NO: 16, wherein] selected from the group consisting of:

a) nucleotides 65-4163 of SEQ ID NO:7,

b) SEQ ID NO:15, and

- c) a DNA sequence which hybridizes with SEQ ID NO:15 or nucleotides 65-4163 of SEQ ID NO:7 under conditions comprising hybridization [is carried out] in a solution comprising 50% formamide, 5X 8SC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 μ g/ml carrier DNA, and [hybridization washes are performed] washing in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes.
- 45. (Reiterated) The DNA sequence according to Claim 44, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.



- 46. (Reiterated) The DNA sequence according to Claim 45, wherein said transport signal encoding sequence comprises a plastid transit peptide.
- 47. (Reiterated) The DNA sequence according to Claim 44, further comprising a transport signal encoding sequence for a signal peptide which provides for transport across the rough endoplasmic reticulum.
- 48. (Reiterated) The DNA sequence according to Claim 47, wherein said sequence further comprises, 3' to said open reading frame, a vacuolar localization signal.
- 49. (Reiterated) The DNA sequence of Claim 44 wherein said open reading frame is from a bacterial gene.

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- 50: (Amended) The DNA sequence of Claim 49 wherein said <u>bacterial</u> gene is selected from the group consisting of ORF438, tyrA, pig, and tna.
- 51. (Reiterated) A DNA construct comprising a DNA sequence of Claim 44.

(Amended) The DNA construct of Claim-51 wherein said cotton plant cell is a cotton fiber cell.

- 53. (Reiterated) A plant cell comprising a DNA construct of Claim 51.
- 54. (Reiterated) A plant comprising a plant cell of Claim 53.

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(Amended) The DNA sequence according to Claim 44 wherein said <u>transcriptional</u> factor is obtained by probing a genomic library derived from a plant fiber tissue [is cotton fiber tissue].

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57. (Twice Amended) A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional factor functional in a cotton fiber cell and an open reading frame encoding an enzyme in the biosynthetic pathway of a pigment, wherein said transcriptional factor is [obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from the cDNA sequence shown in SEQ ID NO: 1 or SEQ.ID NO: 7 or SEQ ID NO: 16, wherein] selected from the group consisting of:

a) nucleotides 65-4163 of SEQ ID NO:7,

b) SEQ ID NO:15, and

c) a DNA sequence which hybridizes with SEQ ID NO:15 or nucleotides 65-4163 of SEQ ID NO:7 under conditions comprising hybridization [is carried out] in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 μ g/ml carrier DNA, and [hybridization washes are performed] washing in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes.

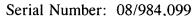
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59. (Amended) A DNA sequence comprising a transcriptional factor functional in a cotton [fiber] plant cell, wherein said transcriptional factor is [obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from a cDNA sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7,







SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO:15 and SEQ ID NO: 16, wherein] selected from the group consisting of:

a) nucleotides 65-4163 of SEQ ID NO:7,

b) SEQ ID NO:15, and

c) a DNA sequence which hybridizes with up to the full length of SEQ ID NO:15 or nucleotides 65-4163 of SEQ ID NO:7 under conditions comprising hybridization [is carried out] in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and [hybridization washes are performed] washing in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes.

Cancel Claim 60.

61. (Allowable) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in SEQ ID NO: 11.

Cancel Claims 62-64.

Please add the following new claims:

65. (New) An isolated DNA comprising the cotton transcriptional sequence shown in SEQ ID NO:7.

66. (New) An isolated DNA comprising the cotton transcriptional sequence shown in SEQ ID NO:15.--.

